



1

SEQUENCE LISTING

<110> Kock, Michael
Hoeger, Thomas
Kroeger, Burkhard
Otterbach, Bernd
Lubisch, Wilfried
Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586
<141> 1999-06-04

<150> PCT/EP99/03889
<151> 1999-06-04

<160> 33

<170> PatentIn/WordPerfect

<210> 1
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)...(1715)
<223> product is Poly ADP Ribose Polymerase; from brain tissue

<400> 1

cc atg gcg gcg cgg cgg cga cgg acc ggc ggc ggc agg gcg aga 47
Met Ala Ala Arg Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg
1 5 10 15

gca tta aat gaa agc aaa aga gtt aat aat ggc aac acg gct cca gaa 95
Ala Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu
20 25 30

gac tct tcc cct gcc aag aaa act cgt aga tgc cag aga cag gag tcg 143
Asp Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser
35 40 45

aaa aag atg cct gtg gct gga gga aaa gct aat aag gac agg aca gaa 191
Lys Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu
50 55 60

gac aag caa gat gaa tct gtg aag gcc ttg ctg tta aag ggc aaa gct 239
Asp Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala
65 70 75

cct gtg gac cca gag tgt aca gcc aag gtg ggg aag gct cat gtg tat 287
Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
80 85 90 95

tgt gaa gga aat gat gtc tat gat gtc atg cta aat cag acc aat ctc Cys Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu 100 105 110	335
cag ttc aac aac aac aag tac tat ctg att cag cta tta gaa gat gat Gln Phe Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp 115 120 125	383
gcc cag agg aac ttc agt gtt tgg atg aga tgg ggc cga gtt ggg aaa Ala Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys 130 135 140	431
atg gga cag cac agc ctg gtg gct tgt tca ggc aat ctc aac aag gcc Met Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala 145 150 155	479
aag gaa atc ttt cag aag aaa ttc ctt gac aaa acg aaa aac aat tgg Lys Glu Ile Phe Gln Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp 160 165 170 175	527
gaa gat cga gaa aag ttt gag aag gtg cct gga aaa tat gat atg cta Glu Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu 180 185 190	575
cag atg gac tat gcc acc aat act cag gat gaa gag gaa aca aag aaa Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Thr Lys Lys 195 200 205	623
gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt Glu Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu 210 215 220	671
cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa Arg Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu 225 230 235	719
gaa atg atg atg gaa atg aag tat aat acc aag aaa gcc cca ctt ggg Glu Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly 240 245 250 255	767
aag ctg aca gtg gca caa atc aag gca ggt tac cag tct ctt aag aag Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys 260 265 270	815
att gag gat tgt att cgg gct ggc cag cat gga cga gct ctc atg gaa Ile Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu 275 280 285	863
gca tgc aat gaa ttc tac acc agg att ccg cat gac ttt gga ctc cgt Ala Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg 290 295 300	911
act cct cca cta atc cgg aca cag aag gaa ctg tca gaa aaa ata caa Thr Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln 305 310 315	959
tta cta gag gct ttg gga gac att gaa att gct att aag ctg gtg aaa Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys 320 325 330 335	1007

aca gag cta caa agc cca gaa cac cca ttg gac caa cac tat aga aac		1055	
Thr Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn			
340	345	350	
cta cat tgt gcc ttg cgc ccc ctt gac cat gaa agt tac gag ttc aaa		1103	
Leu His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys			
355	360	365	
gtg att tcc cag tac cta caa tct acc cat gct ccc aca cac agc gac		1151	
Val Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp			
370	375	380	
tat acc atg acc ttg ctg gat ttg ttt gaa gtg gag aag gat ggt gag		1199	
Tyr Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu			
385	390	395	
aaa gaa gcc ttc aga gag gac ctt cat aac agg atg ctt cta tgg cat		1247	
Lys Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His			
400	405	410	415
ggt tcc agg atg agt aac tgg gtg gga atc ttg agc cat ggg ctt cga		1295	
Gly Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg			
420	425	430	
att gcc cca cct gaa gct ccc atc aca ggt tac atg ttt ggg aaa gga		1343	
Ile Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly			
435	440	445	
atc tac ttt gct gac atg tct tcc aag agt gcc aat tac tgc ttt gcc		1391	
Ile Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala			
450	455	460	
tct cgc cta aag aat aca gga ctg ctg ctc tta tca gag gta gct cta		1439	
Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Ser Glu Val Ala Leu			
465	470	475	
ggt cag tgt aat gaa cta cta gag gcc aat cct aag gcc gaa gga ttg		1487	
Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu			
480	485	490	495
ctt caa ggt aaa cat agc acc aag ggg ctg ggc aag atg gct ccc agt		1535	
Leu Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser			
500	505	510	
tct gcc cac ttc gtc acc ctg aat ggg agt aca gtg cca tta gga cca		1583	
Ser Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro			
515	520	525	
gca agt gac aca gga att ctg aat cca gat ggt tat acc ctc aac tac		1631	
Ala Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr			
530	535	540	
aat gaa tat att gta tat aac ccc aac cag gtc cgt atg cgg tac ctt		1679	
Asn Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu			
545	550	555	
tta aag gtt cag ttt aat ttc ctt cag ctg tgg tga atgttgatat		1725	
Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp			
560	565	570	

taaataaacc agagatctga tcttcaagca agaaaataag cagtgttgta cttgtgaatt 1785
 ttgtgatatt ttatgtataaaaactgtac aggtctaaaa aaaaaaaaaaaa aaaaaaaaa 1843

<210> 2
 <211> 570
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ala Ala Arg Arg Arg Ser Thr Gly Gly Gly Arg Ala Arg Ala
 1 5 10 15

Leu Asn Glu Ser Lys Arg Val Asn Asn Gly Asn Thr Ala Pro Glu Asp
 20 25 30

Ser Ser Pro Ala Lys Lys Thr Arg Arg Cys Gln Arg Gln Glu Ser Lys
 35 40 45

Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
 50 55 60

Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Lys Gly Lys Ala Pro
 65 70 75 80

Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
 85 90 95

Glu Gly Asn Asp Val Tyr Asp Val Met Leu Asn Gln Thr Asn Leu Gln
 100 105 110

Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
 115 120 125

Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
 130 135 140

Gly Gln His Ser Leu Val Ala Cys Ser Gly Asn Leu Asn Lys Ala Lys
 145 150 155 160

Glu Ile Phe Gln Lys Lys Phe Leu Asp Lys Thr Lys Asn Asn Trp Glu
 165 170 175

Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
 180 185 190

Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Thr Lys Lys Glu
 195 200 205

Glu Ser Leu Lys Ser Pro Leu Lys Pro Glu Ser Gln Leu Asp Leu Arg
 210 215 220

Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
 225 230 235 240

Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
 245 250 255

Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
 260 265 270

Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
 275 280 285

Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
 290 295 300

Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
 305 310 315 320

Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
 325 330 335

Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
 340 345 350

His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
 355 360 365

Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
 370 375 380

Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
 385 390 395 400

Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
 405 410 415

Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
 420 425 430

Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
 435 440 445

Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
 450 455 460

Arg Leu Lys Asn Thr Gly Leu Leu Leu Ser Glu Val Ala Leu Gly
 465 470 475 480

Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu Leu
 485 490 495

Gln Gly Lys His Ser Thr Lys Gly Leu Gly Lys Met Ala Pro Ser Ser
 500 505 510

Ala His Phe Val Thr Leu Asn Gly Ser Thr Val Pro Leu Gly Pro Ala
 515 520 525

Ser Asp Thr Gly Ile Leu Asn Pro Asp Gly Tyr Thr Leu Asn Tyr Asn
 530 535 540

Glu Tyr Ile Val Tyr Asn Pro Asn Gln Val Arg Met Arg Tyr Leu Leu
 545 550 555 560

Lys Val Gln Phe Asn Phe Leu Gln Leu Trp
 565 570

<210> 3
 <211> 2265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (242)...(1843)
 <223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 3

tggactgg	cgcctgactc	ggcctgcccc	agcctctgct	tcacccact	ggtggccaaa	60
tagccatgt	ctaattcccc	acacaagctc	atccccggcc	tctgggattg	ttggaaattc	120
tctccataat	tcacgcctga	ggctcatgga	gagttgctag	acctggact	gccctggag	180
gcccacacaa	ccaggccggg	tggcagccag	gacctctccc	atgtccctgc	tttttttggc	240
c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag						286
Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu						
1	5	10	15			
aag aag aag ggc	cg	gca gga	agg gag	gac ccc	ttc cgc tcc	334
Lys Lys Lys	Gly Arg	Gln Ala	Gly Arg	Glu Glu	Asp Pro	Phe Arg Ser
20	25	30				
acc gct gag gcc	ctc aag	gcc ata ccc	gca gag aag	cg	ata atc cgc	382
Thr Ala Glu	Ala Leu	Lys Ala Ile	Pro Ala	Glu Lys	Arg Ile	Ile Arg
35	40	45				
gtg gat cca aca	tgt cca	ctc agc agc	aac ccc	ggg acc	cag gtg tat	430
Val Asp Pro	Thr Cys	Pro Leu	Ser Ser	Asn Pro	Gly Thr	Gln Val Tyr
50	55	60				
gag gac tac aac	tgc acc	ctg aac	cag acc	aatc	gag aac aac aac	478
Glu Asp Tyr	Asn Cys	Thr Leu	Asn Gln	Thr Asn	Ile Glu Asn Asn Asn	
65	70	75				
aac aag ttc tac	atc atc	cag ctg	ctc caa	gac agc	aac cgc ttc ttc	526
Asn Lys	Phe Tyr	Ile Ile	Gln Leu	Leu Gln	Asp Ser Asn Arg Phe Phe	
80	85	90	95			
acc tgc tgg aac	cgc tgg	ggc cgt	gtg gga	gag gtc	ggc cag tca aag	574
Thr Cys	Trp Asn	Arg Trp	Gly Arg	Val Gly	Glu Val Gly Gln Ser Lys	
100	105	110				
atc aac cac ttc	aca agg	cta gaa	gat gca	aag gac	ttt gag aag	622
Ile Asn His	Phe Thr	Arg Leu	Glu Asp	Ala Lys	Lys Asp Phe Glu Lys	
115	120	125				
aaa ttt cgg gaa	aag acc	aag aac	aac tgg	gca gag	cg gac cac ttt	670
Lys Phe Arg	Glu Lys	Thr Lys	Asn Asn	Trp Ala	Glu Arg Asp His Phe	
130	135	140				
gtg tct cac ccg	ggc aag	tac aca	ctt atc	gaa gta	cag gca gag gat	718
Val Ser His	Pro Gly	Lys Tyr	Thr Leu	Ile Glu	Val Gln Ala Glu Asp	

145	150	155	
gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg act Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr 160 165 170 175			766
gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag aag Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys 180 185 190			814
ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg gcc Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala 195 200 205			862
ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc aag Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys 210 215 220			910
caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag gcc Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala 225 230 235			958
ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc tca Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser 240 245 250 255			1006
cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc ccg His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro 260 265 270			1054
ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg ctg Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu 275 280 285			1102
gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct gag Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu 290 295 300			1150
cag gag aag acg gtg gag gag gtc cca cac ccc ctg gac cga gac tac Gln Glu Lys Thr Val Glu Val Pro His Pro Leu Asp Arg Asp Tyr 305 310 315			1198
cag ctt ctc aag tgc cag ctg cag cta gac tct gga gca cct gag Gln Leu Leu Lys Cys Gln Leu Gln Leu Asp Ser Gly Ala Pro Glu 320 325 330 335			1246
tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac agg Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg 340 345 350			1294
tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag gaa Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu 355 360 365			1342
gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg tgg Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp 370 375 380			1390
cat ggc acc aac atg gcc gtg gtg gcc atc ctc act agt ggg ctc			1438

His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu			
385	390	395	
cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac ttt			1486
Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe			
400	405	410	415
gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag tgt			1534
Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys			
420	425	430	
ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg ggc			1582
Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly			
435	440	445	
aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca cct			1630
Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro			
450	455	460	
cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat ccg			1678
Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro			
465	470	475	
acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg ccc			1726
Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro			
480	485	490	495
cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc tcc			1774
Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser			
500	505	510	
cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc tac			1822
Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr			
515	520	525	
ctg ctg gag gtc cac ctc tga gtgccccccc tgccccccgg ggtcctgcaa			1873
Leu Leu Glu Val His Leu			
530			
ggctggactg tgatttcaa tcatcctgcc catctctggt acccctatat cactcctttt			1933
tttcaagaat acaatacggt gttgttaact atagtcacca tgctgtacaa gatccctgaa			1993
cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc			2053
cagcccatgg taaccagcat ttgactctt acttgtataa gggcagctt tataggttcc			2113
acatgttaagt gagatcatgc agtgttgtc tttctgtgcc tggcttattt cactcagcat			2173
aatgtgcacc gggttcaccc atgtttcat aaatgacaag atttcctcct taaaaaaaaa			2233
aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa			2265

<210> 4
 <211> 533
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro Glu Lys
 1 5 10 15

Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 20 25 30

Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile Arg Val
 35 40 45

Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val Tyr Glu
 50 55 60

Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn Asn Asn
 65 70 75 80

Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe Phe Thr
 85 90 95

Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Ile
 100 105 110

Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys Lys
 115 120 125

Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His Phe Val
 130 135 140

Ser His Pro Gly Lys Tyr Thr Leu Glu Val Gln Ala Glu Asp Glu
 145 150 155 160

Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg Thr Val
 165 170 175

Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln Lys Leu
 180 185 190

Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met Ala Leu
 195 200 205

Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys Gln
 210 215 220

Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Leu
 225 230 235 240

Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser His
 245 250 255

Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro Pro
 260 265 270

Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu Val
 275 280 285

Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser Glu Gln
 290 295 300

10

Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
 305 310 315 320

Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
 325 330 335

Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
 340 345 350

Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
 355 360 365

Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
 370 375 380

Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400

Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415

Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys Cys Gly
 420 425 430

Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
 435 440 445

Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460

Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
 465 470 475 480

Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
 485 490 495

Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Ser Thr Phe Ser Gln
 500 505 510

Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg Tyr Leu
 515 520 525

Leu Glu Val His Leu
 530

<210> 5
<211> 2265
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (221)...(1843)
<223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 5

tgggactggc cgccctgactc ggcctgcccc agcctctgct tcaccccaact ggtggccaaa

60

11

tagccgatgt ctaatcccc acacaagctc atccccggcc tctgggattt ttgggaattc	120
tctccctaattcacgcctga ggctcatgga gagttgctag acctggact gccctggag	180
gcccacacaa ccaggccggg tggcagccag gacctctccc atg tcc ctg ctt ttc Met Ser Leu Leu Phe	235
1 5	
ttg gcc atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro	283
10 15 20	
gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc Glu Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg	331
25 30 35	
tcc acc gct gag gcc ctc aag gcc ata ccc gca gag aag cgc ata atc Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile	379
40 45 50	
cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val	427
55 60 65	
tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn	475
70 75 80 85	
aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe	523
90 95 100	
ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser	571
105 110 115	
aag atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu	619
120 125 130	
aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His	667
135 140 145	
ttt gtg tct cac ccc ggc aag tac aca ctt atc gaa gta cag gca gag Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu	715
150 155 160 165	
gat gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg	763
170 175 180	
act gtg act aag cgg gtg cag ccc tgc tcc ctg gac cca gcc acg cag Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln	811
185 190 195	
aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met	859
200 205 210	

gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc		907
Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser		
215 220 225		
aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag		955
Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu		
230 235 240 245		
gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc		1003
Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser		
250 255 260		
tca cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc		1051
Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro		
265 270 275		
ccg ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg		1099
Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu		
280 285 290		
ctg gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct		1147
Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser		
295 300 305		
gag cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac		1195
Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp		
310 315 320 325		
tac cag ctt ctc aag tgc cag ctg cag ctg cta gac tct gga gca cct		1243
Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro		
330 335 340		
gag tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac		1291
Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His		
345 350 355		
agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag		1339
Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu		
360 365 370		
gaa gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg		1387
Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu		
375 380 385		
tgg cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctc act agt ggg		1435
Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly		
390 395 400 405		
ctc cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac		1483
Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr		
410 415 420		
ttt gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag		1531
Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys		
425 430 435		
tgt ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg		1579
Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu		
440 445 450		

ggc aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro 455 460 465	1627
cct cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp 470 475 480 485	1675
ccg acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val 490 495 500	1723
ccc cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Thr Phe 505 510 515	1771
tcc cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg 520 525 530	1819
tac ctg ctg gag gtc cac ctc tga gtgccccccc tgtcccccg ggtcctgcaa Tyr Leu Leu Glu Val His Leu 535 540	1873
ggctggactg tgatttcaa tcatcctgcc catctctggt acccctatat cactccttt tttcaagaat acaatacggt gttgttaact atagtcacca tgctgtacaa gatccctgaa cttatgcctc ctaactgaaa tttgtattc tttgacacat ctgcccagtc cctctcctcc cagccccatgg taaccagcat ttgactctt acttgtataa gggcagctt tataggttcc acatgttaagt gagatcatgc agtgtttgtc tttctgtgcc tggcttattt cactcagcat aatgtgcacc gggttcaccc atgtttcat aaatgacaag atttcctcct taaaaaaaa aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa	1933 1993 2053 2113 2173 2233 2265

<210> 6
<211> 540
<212> PRT
<213> Homo sapiens

<400> 6

Met Ser Leu Leu Phe Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val
1 5 10 15

Gln Thr Glu Gly Pro Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu
20 25 30

Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
35 40 45

Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
50 55 60

Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr

65	70	75	80
Asn Ile Glu Asn Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln			
85	90	95	
Asp Ser Asn Arg Phe Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly			
100	105	110	
Glu Val Gly Gln Ser Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala			
115	120	125	
Lys Lys Asp Phe Glu Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp			
130	135	140	
Ala Glu Arg Asp His Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile			
145	150	155	160
Glu Val Gln Ala Glu Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp			
165	170	175	
Arg Gly Pro Val Arg Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu			
180	185	190	
Asp Pro Ala Thr Gln Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met			
195	200	205	
Phe Lys Asn Thr Met Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro			
210	215	220	
Leu Gly Lys Leu Ser Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu			
225	230	235	240
Glu Ala Leu Glu Glu Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser			
245	250	255	
Leu Glu Glu Leu Ser Ser His Phe Tyr Thr Val Ile Pro His Asn Phe			
260	265	270	
Gly His Ser Gln Pro Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala			
275	280	285	
Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala			
290	295	300	
Leu Gln Ala Val Ser Glu Gln Glu Lys Thr Val Glu Glu Val Pro His			
305	310	315	320
Pro Leu Asp Arg Asp Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu			
325	330	335	
Asp Ser Gly Ala Pro Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln			
340	345	350	
Thr Gly Ser Asn His Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val			
355	360	365	
Asn Gln Glu Gly Glu Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly			
370	375	380	

15

Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
 385 390 395 400
 Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val
 405 410 415
 Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
 420 425 430
 Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
 435 440 445
 Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
 450 455 460
 Ser Leu Lys Ser Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
 465 470 475 480
 His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
 485 490 495
 Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
 500 505 510
 Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser
 515 520 525
 Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu
 530 535 540

<210> 7
 <211> 1740
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (112) ... (1710)

<400> 7

cccggctttc acttttctg ctgcctcgaa gAACACCTCG agCCAactGC ttcctaactC 60
 agggtgggca gaactgacgg gatctaagct tctgcatactc tgaggagaac C atG gCT 117
 Met Ala
 1
 cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga 165
 Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
 5 10 15
 caa ggg aca gag gag gac agc ttc cgg tcc act gcc gag gct ctc 213
 Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
 20 25 30
 aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt 261
 Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
 35 40 45 50

cca ttc agc cg aac ccc ggg ata cag gtc cac gag gac tat gac tgt Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys 55 60 65	309
acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe Tyr Ile 70 75 80	357
atc caa ctg ctg gag gag ggt agt cgc ttc tgc tgg aat cgc tgg Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp 85 90 95	405
ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys 100 105 110	453
ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu Lys Thr 115 120 125 130	501
aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys 135 140 145	549
tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val 150 155 160	597
gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtc Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val 165 170 175	645
gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn 180 185 190	693
atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu 195 200 205 210	741
gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala 215 220 225	789
cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Ala Met Lys Asn Pro 230 235 240	837
aca ggg gat ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr 245 250 255	885
gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser 260 265 270	933
cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp 275 280 285 290	981

atc gag ttg gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu 295 300 305	1029
aaa gtg gaa gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu 310 315 320	1077
agg tgc cag ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Tyr Lys Ala 325 330 335	1125
ata cag acc tac ctg aaa cag act ggc aac agc tac agg tgc cca aac Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn 340 345 350	1173
ctg cgg cat gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe 355 360 365 370	1221
cag gcc cac tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr 375 380 385	1269
aat gtg gcc gtg gtc gcc atc ctc acc agt ggg ctc cga atc atg Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met 390 395 400	1317
cca cac tcg ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu 405 410 415	1365
aac agc aag tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His 420 425 430	1413
cag gtg ggc tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His 435 440 445 450	1461
cac atc acc atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe 455 460 465	1509
gac agc gtc atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp 470 475 480	1557
att gaa ctt gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro 485 490 495	1605
cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu 500 505 510	1653
tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu 515 520 525 530	1701

att cac ctc taagctgctt gccctcccta ggtccaagcc 1740
 Ile His Leu

<210> 8
 <211> 533
 <212> PRT
 <213> Mus musculus

<400> 8

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
 1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
 145 150 155 160

Ala Val Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg
 165 170 175

Thr Val Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile
 180 185 190

Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met
 195 200 205

Asn Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln
 210 215 220

Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys
 225 230 235 240

Asn Pro Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe
 245 250 255

Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile
 260 265 270
 Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu
 275 280 285
 Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu
 290 295 300
 Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
 305 310 315 320
 Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
 325 330 335
 Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
 340 345 350
 Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
 355 360 365
 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
 370 375 380
 Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400
 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415
 Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
 420 425 430
 Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
 435 440 445
 Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460
 Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala
 465 470 475 480
 Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln
 485 490 495
 Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln
 500 505 510
 Ser Glu Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu
 515 520 525
 Leu Glu Ile His Leu
 530

<210> 9
 <211> 1587
 <212> DNA
 <213> Mus musculus

<220>
<221> CDS
<222> (1)...(1584)

<400> 9

atg gct cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag	48
Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys	
1 5 10 15	
cag cga caa ggg aca gag gag gag gac ttc cgg tcc act gcc gag	96
Gln Arg Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	
20 25 30	
gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc	144
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro	
35 40 45	
tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat	192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	
50 55 60	
gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aag ttc	240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe	
65 70 75 80	
tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat	288
Tyr Ile Ile Gln Leu Leu Glu Glu Ser Arg Phe Phe Cys Trp Asn	
85 90 95	
cgc tgg ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc	336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	
100 105 110	
acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag	384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu	
115 120 125	
aag act aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc	432
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
130 135 140	
aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
145 150 155 160	
gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtg gtc aag ccc	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
165 170 175	
tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
180 185 190	
aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
195 200 205	
aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc	672

Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe			
210	215	220	
gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc aca ggg gat			720
Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp			
225	230	235	240
ggc cag agc ctg gaa gag ctc tcc tgc ttc tac act gtc atc cca			768
Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro			
245	250	255	
cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc cct gat gtg			816
His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val			
260	265	270	
ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac atc gag ttg			864
Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu			
275	280	285	
gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag aaa gtg gaa			912
Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu			
290	295	300	
gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc agg tgc cag			960
Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln			
305	310	315	320
ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca ata cag acc			1008
Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr			
325	330	335	
tac ctg aaa cag act ggc aac agc tac agg tgc cca aac ctg cgg cat			1056
Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His			
340	345	350	
gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc cag gcc cac			1104
Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His			
355	360	365	
tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc aat gtg gcc			1152
Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala			
370	375	380	
gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg cca cac tcg			1200
Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser			
385	390	395	400
ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag aac agc aag			1248
Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys			
405	410	415	
tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac cag gtg ggc			1296
Ser Ala Gly Tyr Val Thr Met His Cys Gly Gly His Gln Val Gly			
420	425	430	
tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac cac atc acc			1344
Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr			
435	440	445	

atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt gac agc gtc Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val 450 455 460	1392
atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac att gaa ctt Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu 465 470 475 480	1440
gaa ctg gat ggg cag ccg gtg gtg ccc caa ggc ccg cct gtg cag Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln 485 490 495	1488
tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa tac ctc ata Cys Pro Ser Phe Lys Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile 500 505 510	1536
tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag att cac ctc Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu 515 520 525	1584
taa	1587

<210> 10
<211> 528
<212> PRT
<213> Mus musculus

<400> 10

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys 1 5 10 15
Gln Arg Gln Gly Thr Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu 20 25 30
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro 35 40 45
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr 50 55 60
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Lys Phe 65 70 75 80
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn 85 90 95
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe 100 105 110
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Phe Trp Glu 115 120 125
Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro 130 135 140
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu 145 150 155 160

Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro
 165 170 175

 Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser
 180 185 190

 Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys
 195 200 205

 Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala Arg Gly Phe
 210 215 220

 Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro Thr Gly Asp
 225 230 235 240

 Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr Val Ile Pro
 245 250 255

 His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser Pro Asp Val
 260 265 270

 Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu Ala Asp Ile Glu Leu
 275 280 285

 Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Lys Val Glu
 290 295 300

 Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu Arg Cys Gln
 305 310 315 320

 Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala Ile Gln Thr
 325 330 335

 Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn Leu Arg His
 340 345 350

 Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe Gln Ala His
 355 360 365

 Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr Asn Val Ala
 370 375 380

 Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser
 385 390 395 400

 Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys
 405 410 415

 Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His His Ile Thr
 420 425 430 430

 Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His His Ile Thr
 435 440 445

 Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
 450 455 460

 Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
 465 470 475 480

Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 485 490 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 500 505 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 515 520 525

<210> 11
<211> 18
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (2)...(6), (9)...(11)
<223> any amino acid; residues 3 to 6 may be present or absent

<220>
<221> VARIANT
<222> (7)
<223> amino acid residue 7 is either Ser or Thr

<400> 11

Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr
 1 5 10 15

Phe Ala

<210> 12
<211> 25
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (1), (14)
<223> amino acid residues 1 and 14 are either Ser or Thr

<220>
<221> VARIANT
<222> (2), (7), (9)...(13), (16)...(18)
<223> may be any amino acid; 10-13 may be present or absent

<220>
<221> VARIANT
<222> (6)
<223> amino acid residue 6 is either Ile or Val

<400> 12

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Gly Xaa
 1 5 10 15

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala
 20 25

<210> 13
 <211> 49
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (6), (16), (29)
 <223> Ser or Thr

<220>
 <221> VARIANT
 <222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)
 <223> may be any amino acid; residues 25-28 may be present or absent

<220>
 <221> VARIANT
 <222> 21
 <223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa
 35 40 45

Tyr

<210> 14
 <211> 22
 <212> PRT
 <213> artificial sequence

<220>
 <223> leucine zipper motif

<220>
 <221> VARIANT
 <222> (1)
 <223> Leu or Val

<220>
<221> VARIANT
<222> (2)...(7), (9)...(14), (16)...(21)
<223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
20

<210> 15
<211> 37
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 1

<220>
<221> VARIANT
<222> (21)
<223> Asp or Glu

<220>
<221> VARIANT
<222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)
<223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
1 5 10 15

Gln Leu Leu Xaa
20 25 30

Trp Gly Arg Val Gly
35

<210> 16
<211> 29
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 2

<220>
<221> VARIANT
<222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)
<223> may be any amino acid

<400> 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
 1 5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
 20 25

<210> 17
<211> 44
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 3

<220>
<221> VARIANT
<222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)
<223> may be any amino acid

<220>
<221> VARIANT
<222> (4)
<223> Ile or Leu

<400> 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu
 20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Leu
 35 40

<210> 18
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 4

<220>
<221> VARIANT
<222> (4), (8), (11)...(13)
<223> may be any amino acid

<400> 18

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro
 1 5 10 15

<210> 19
<211> 17
<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 5

<220>

<221> VARIANT

<222> (2)...(4), (6)...(7), (9), (13), (15)...(16)

<223> may be any amino acid

<400> 19

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
 1 5 10 15

Leu

<210> 20

<211> 11

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 6

<220>

<221> VARIANT

<222> (2)...(4), (6)

<223> may be any amino acid

<400> 20

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 1 5 10

<210> 21

<211> 28

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 7

<220>

<221> VARIANT

<222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)

<223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val
 20 25

<210> 22
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> part-sequence motif 8

<220>
<221> VARIANT
<222> (2)
<223> Tyr or Phe

<220>
<221> VARIANT
<222> (3)...(4), (6)...(8), (10)...(13)
<223> may be any amino acid

<400> 22

Glu	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Tyr	Leu	Leu
1					5				10				15	

<210> 23
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 23

Met	Ala	Ala	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala
1						5			10			15		

Leu	Asn	Glu	Ser
		20	

<210> 24
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 24

Lys	Thr	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg
1					5				10				15		

Asn	Leu	His	Cys
		20	

30

<210> 25
<211> 21
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
1 5 10 15

Ala Glu Ala Leu Lys
20

<210> 26
<211> 20
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
1 5 10 15

Glu Ala Leu Lys
20

<210> 27
<211> 19
<212> PRT
<213> artificial sequence

<220>
<223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Leu Lys

<210> 28
<211> 19
<212> PRT
<213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
1 5 10 15

Ala Met Lys

<210> 29
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> NAD+ binding domain

<220>
<221> VARIANT
<222> (2)...(4)
<223> may be any amino acid residue

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly
1 5

<210> 30
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> PARP zinc finger sequence motif

<220>
<221> VARIANT
<222> (2)...(3), (5)...(34), (36)...(37)
<223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa
1 5 10 15

Xaa
20 25 30

Xaa Xaa His Xaa Xaa Cys
35

<210> 31
<211> 10
<212> PRT
<213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
1 5 10

<210> 32

<211> 39
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) . . . (39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg
Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10

39

<210> 33
<211> 13
<212> PRT
<213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
1 5 10